

SEQUENCE LISTING

<110> Curtis, Rory A.J.

<120> 8099, 46455, 54414, 53763, 67076, 67102, 44181,
67084FL, AND 67084 ALT, HUMAN PROTEINS AND METHODS OF
USE THEREOF

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<151> 2000-12-15

<150> US 60/256,588

<151> 2000-12-18

<150> US 60/258,028

<151> 2000-12-21

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<213> Homo sapiens

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<221> CDS

<222> (180)...(2033)

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Ser	Tyr	Thr	Val	Leu	Ile	Val	Gly	Arg	Ile	Ala	Ile	Gly	Val	Ser	Ile		
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Ile	Gly	Ile	Leu	Ser	Ala	Tyr	Ile	Ser	Asn	Tyr	Ala	Phe	Ala	Asn	Val		
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Phe	His	Gly	Trp	Lys	Tyr	Met	Phe	Gly	Leu	Val	Ile	Pro	Leu	Gly	Val		
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1955


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Top of page

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 Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly Gly Ala
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T02F "E23400"

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Asp Asp Gly Pro Val Pro Gly Thr Pro Gly Leu Pro Gly Ser Thr Gly	
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aac ccg aag tcc gag gag ccc gag gtc ccg gac cag gag ggg ctg cag	144
Asn Pro Lys Ser Glu Glu Pro Glu Val Pro Asp Gln Glu Gly Leu Gln	
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cgc atc acc ggc ctg tct ccc ggc cgt tcg gct ctc ata gtg gcg gtg	192
Arg Ile Thr Gly Leu Ser Pro Gly Arg Ser Ala Leu Ile Val Ala Val	
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ctg tgc tac atc aat ctc ctg aac tac atg gac cgc ttc acc gtg gct	240
Leu Cys Tyr Ile Asn Leu Leu Asn Tyr Met Asp Arg Phe Thr Val Ala	
65 70 75 80	
ggc gtc ctt ccc gac atc gag cag ttc ttc aac atc ggg gac agt agc	288
Gly Val Leu Pro Asp Ile Glu Gln Phe Phe Asn Ile Gly Asp Ser Ser	
85 90 95	
tct ggg ctc atc cag acc gtg ttc atc tcc agt tac atg gtg ttg gca	336
Ser Gly Leu Ile Gln Thr Val Phe Ile Ser Ser Tyr Met Val Leu Ala	
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cct gtg ttt ggc tac ctg ggt gac agg tac aat cgg aag tat ctc atg	384
Pro Val Phe Gly Tyr Leu Gly Asp Arg Tyr Asn Arg Lys Tyr Leu Met	
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Cys Gly Gly Ile Ala Phe Trp Ser Leu Val Thr Leu Gly Ser Ser Phe	

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100443 22342037

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Thr Ala Ile Phe Ile Glu Ala Asp Arg Arg Arg Ala Gln Leu His Val
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Gln Gly Leu Leu His Glu Ala Gly Ser Thr Asp Asp Arg Ile Val Val
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ccc cag cgg ggc cgc tcc acc cgc gtg ccc gtg gcc agt gtg ctc atc 1584
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 Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile Arg Leu Phe Asn Phe Ser
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 70 75 80
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 Phe Glu Thr Ile Leu Leu Gly Tyr Leu Ser Tyr Lys Gly Asn Ile Trp
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100442
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100463-200T

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T004001

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 His Asn Tyr Tyr Glu Asp Ala Lys Ala Tyr Gly Phe Lys Asn Lys Leu
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 740 745 750
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 785 790 795 800
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 Ser Glu Ser Arg Lys Ile Ala Ser Gln Ser Gln Ile Ser Ile Ser Val
 945 950 955 960
 Glu Glu Trp Glu Asp Thr Lys Asp Ser Lys Glu Gln Gly His His Arg

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ttt cga gat ttg ctg cta ggg gac caa gga tgg caa aac gat gac aga      96
Phe Arg Asp Leu Leu Leu Gly Asp Gln Gly Trp Gln Asn Asp Asp Arg
                20                      25              30

gta caa gtt gaa ttc tat atg aat gaa aat aca ttt aaa gaa aga cta      144
Val Gln Val Glu Phe Tyr Met Asn Glu Asn Thr Phe Lys Glu Arg Leu
                35                      40              45

aaa tta ttt ttc ata aaa aac cag aga tca agt cta agg ata cgc ctg      192
Lys Leu Phe Phe Ile Lys Asn Gln Arg Ser Ser Leu Arg Ile Arg Leu
   50                               55              60

ttc aat ttt tct ctg aaa tta cta agc tgc tta tta tac ata atc cga      240
Phe Asn Phe Ser Leu Lys Leu Leu Ser Cys Leu Leu Tyr Ile Ile Arg
   65                               70              75              80

gta cta cta gaa aac cct tca caa gga aat gaa tgg tct cat atc ttt      288
Val Leu Leu Glu Asn Pro Ser Gln Gly Asn Glu Trp Ser His Ile Phe
                85                      90              95

tgg gtg aac aga agt cta cct ttg tgg ggc tta cag gtt tca gtg gca      336
Trp Val Asn Arg Ser Leu Pro Leu Trp Gly Leu Gln Val Ser Val Ala
                100                     105              110

ttg ata agt ctg ttt gaa aca ata tta ctt ggt tat ctt agt tat aag      384
Leu Ile Ser Leu Phe Glu Thr Ile Leu Leu Gly Tyr Leu Ser Tyr Lys

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gac cta ttg aga gca aag atg gat gac gct gag gcc tgt ttt att ctc 1152
 Asp Leu Leu Arg Ala Lys Met Asp Asp Ala Glu Ala Cys Phe Ile Leu
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agt agc cgt tgt gaa gtg gat agg aca tca tct gat cac caa aca att 1200
 Ser Ser Arg Cys Glu Val Asp Arg Thr Ser Ser Asp His Gln Thr Ile
 385 390 395 400

ttg aga gca tgg gct gtg aaa gat ttt gct cca aat tgt cct ttg tat 1248
 Leu Arg Ala Trp Ala Val Lys Asp Phe Ala Pro Asn Cys Pro Leu Tyr
 405 410 415

gtc cag ata tta aag cct gaa aat aaa ttt cac atc aaa ttt gct gat 1296
 Val Gln Ile Leu Lys Pro Glu Asn Lys Phe His Ile Lys Phe Ala Asp
 420 425 430

cat gtt gtt tgt gaa gaa gag ttt aaa tac gcc atg tta gct tta aac 1344
 His Val Val Cys Glu Glu Glu Phe Lys Tyr Ala Met Leu Ala Leu Asn
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tgt ata tgc cca gca aca tct aca ctt att aca cta ctg gtt cat acc 1392
 Cys Ile Cys Pro Ala Thr Ser Thr Leu Ile Thr Leu Leu Val His Thr
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tct aga ggg caa gaa ggc cag caa tcg cca gaa caa tgg cag aag atg 1440
 Ser Arg Gly Gln Glu Gly Gln Gln Ser Pro Glu Gln Trp Gln Lys Met
 465 470 475 480

tac ggt aga tgc tcc ggg aat gaa gtc tac cac att gtt ttg gaa gaa 1488
 Tyr Gly Arg Cys Ser Gly Asn Glu Val Tyr His Ile Val Leu Glu Glu
 485 490 495

agt aca ttt ttt gct gaa tat gaa gga aag agt ttt aca tat gcc tct 1536
 Ser Thr Phe Phe Ala Glu Tyr Glu Gly Lys Ser Phe Thr Tyr Ala Ser
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 Phe His Ala His Lys Lys Phe Gly Val Cys Leu Ile Gly Val Arg Arg
 515 520 525

gag gat aat aaa aac att ttg ctg aat cca ggt cct cga tac att atg 1632
 Glu Asp Asn Lys Asn Ile Leu Leu Asn Pro Gly Pro Arg Tyr Ile Met
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aat tct acg gac ata tgc ttt tat att aat att acc aaa gaa gag aat 1680
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 545 550 555 560

tca gca ttt aaa aac caa gac cag cag aga aaa agc aat gtg tcc agg 1728
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agc atg ggt act gtg gct ata gac ctg caa gat aca agc tgt aga tca 1824
 Ser Met Gly Thr Val Ala Ile Asp Leu Gln Asp Thr Ser Cys Arg Ser
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T.D. Lee "E. coli"

ttc tgg ggc atc gac gag acc gac gtg gag ccc tgc tgc tgg atg acc	1025
Phe Trp Gly Ile Asp Glu Thr Asp Val Glu Pro Cys Cys Trp Met Thr	
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Tyr Arg Gln His Arg Asp Ala Glu Glu Ala Leu Asp Ile Phe Glu Thr	
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ccc gac ctc att ggc ggc gac ccc ggc gac gac gag gac ctg gcg gcc	1121
Pro Asp Leu Ile Gly Gly Asp Pro Gly Asp Asp Glu Asp Leu Ala Ala	
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Lys Arg Leu Gly Ile Glu Asp Ala Ala Gly Leu Gly Gly Pro Asp Gly	
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Lys Ser Gly Arg Trp Arg Arg Leu Gln Pro Arg Met Trp Ala Leu Phe	
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Leu Phe Phe Ile Leu Val Ser Ile Thr Thr Phe Cys Leu Glu Thr His	
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Glu Ala Phe Asn Ile Val Lys Asn Lys Thr Glu Pro Val Ile Asn Gly	
255 260 265	
aca agt gtt gtt cta cag tat gaa att gaa acg gat cct gcc ttg acg	1409
Thr Ser Val Val Leu Gln Tyr Glu Ile Glu Thr Asp Pro Ala Leu Thr	
270 275 280	
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Tyr Val Glu Gly Val Cys Val Val Trp Phe Thr Phe Glu Phe Leu Val	
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cgt att gtt ttt tca ccc aat aaa ctt gaa ttc atc aaa aat ctc ttg	1505
Arg Ile Val Phe Ser Pro Asn Lys Leu Glu Phe Ile Lys Asn Leu Leu	
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Asn Ile Ile Asp Phe Val Ala Ile Leu Pro Phe Tyr Leu Glu Val Gly	
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Leu Ser Gly Leu Ser Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu	
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Arg Val Val Arg Phe Val Arg Ile Leu Arg Ile Phe Lys Leu Thr Arg	
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His Phe Val Gly Leu Arg Val Leu Gly His Thr Leu Arg Ala Ser Thr	
365 370 375	

Ser Lys Ala Ala Lys Asp Val Leu Gly Phe Leu Arg Val Val Arg Phe
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 Val Arg Ile Leu Arg Ile Phe Lys Leu Thr Arg His Phe Val Gly Leu
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 Arg Val Leu Gly His Thr Leu Arg Ala Ser Thr Asn Glu Phe Leu Leu
 370 375 380
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 385 390 395 400
 Tyr Tyr Ala Glu Arg Val Gly Ala Gln Pro Asn Asp Pro Ser Ala Ser
 405 410 415
 Glu His Thr Gln Phe Lys Asn Ile Pro Ile Gly Phe Trp Trp Ala Val
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 Val Thr Met Thr Thr Leu Gly Tyr Gly Asp Met Tyr Pro Gln Thr Trp
 435 440 445
 Ser Gly Met Leu Val Gly Ala Leu Cys Ala Leu Ala Gly Val Leu Thr
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 Ile Ala Met Pro Val Pro Val Ile Val Asn Asn Phe Gly Met Tyr Tyr
 465 470 475 480
 Ser Leu Ala Met Ala Lys Gln Lys Leu Pro Arg Lys Arg Lys Lys His
 485 490 495
 Ile Pro Pro Ala Pro Gln Ala Ser Ser Pro Thr Phe Cys Lys Thr Glu
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 Asp Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu Ser Gly Asp Asp
 530 535 540
 Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile
 545 550 555 560
 Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe
 565 570 575
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 580 585 590
 Lys Gly Tyr Glu Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala
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 Thr Arg His Glu Thr Tyr Arg Ser Thr Leu Lys Thr Leu Pro Gly Thr
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 cgc ctg gcc ctt ctt gcc tcc tcc gag ccc cca ggc gac tgc ttg acc 144
 Arg Leu Ala Leu Leu Ala Ser Ser Glu Pro Pro Gly Asp Cys Leu Thr
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Asp Asn Arg Leu Leu Glu His Asn Arg Ser Val Leu Ser Gly Asp Asp
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 Ser Thr Gly Ser Glu Pro Pro Leu Ser Pro Pro Glu Arg Leu Pro Ile
 545 550 555 560

aga cgc tct agt acc aga gac aaa aac aga aga ggg gaa aca tgt ttc 1728
 Arg Arg Ser Ser Thr Arg Asp Lys Asn Arg Arg Gly Glu Thr Cys Phe
 565 570 575

cta ctg acg aca ggt gat tac acg tgt gct tct gat gga ggg atc agg 1776
 Leu Leu Thr Thr Gly Asp Tyr Thr Cys Ala Ser Asp Gly Gly Ile Arg
 580 585 590

aaa gga tat gaa aaa tcc cga agc tta aac aac ata gcg ggc ttg gca 1824
 Lys Gly Tyr Glu Lys Ser Arg Ser Leu Asn Asn Ile Ala Gly Leu Ala
 595 600 605

ggc aat gct ctg agg ctc tct cca gta aca tca ccc tac aac tct cct 1872
 Gly Asn Ala Leu Arg Leu Ser Pro Val Thr Ser Pro Tyr Asn Ser Pro
 610 615 620

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 Met Phe Arg Arg
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agc ttg aat cgt ttt tgt gct gga gaa gag aaa cga gtt ggc aca cgc 583
 Ser Leu Asn Arg Phe Cys Ala Gly Glu Glu Lys Arg Val Gly Thr Arg
 5 10 15 20

aca gtg ttt gtt ggc aat cat cca gtt tcg gaa aca gaa gct tac att 631
 Thr Val Phe Val Gly Asn His Pro Val Ser Glu Thr Glu Ala Tyr Ile
 25 30 35

gca caa aga ttt tgt gat aat aga ata gtc tca tct aag tat aca ctt 679
 Ala Gln Arg Phe Cys Asp Asn Arg Ile Val Ser Ser Lys Tyr Thr Leu
 40 45 50

The sequence is identical to the sequence in the GenBank database.

tgg aat ttt ctc cca aag aat ctg ttt gaa cag ttt aga aga att gca 727
 Trp Asn Phe Leu Pro Lys Asn Leu Phe Glu Gln Phe Arg Arg Ile Ala
 55 60 65

aat ttt tat ttt ctc ata atc ttc ctt gta cag gtc aca gta gac aca 775
 Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Val Thr Val Asp Thr
 70 75 80

cca act agc cca gtt acc agt gga ctt cca ctt ttc ttt gtt ata act 823
 Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe Phe Val Ile Thr
 85 90 95 100

gtt aca gcc atc aag cag gga tat gag gat tgg ctg aga cac aga gct 871
 Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu Arg His Arg Ala
 105 110 115

gac aat gaa gtc aac aaa agc act gtt tac att att gaa aat gca aag 919
 Asp Asn Glu Val Asn Lys Ser Thr Val Tyr Ile Ile Glu Asn Ala Lys
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cga gtg aga aaa gaa agt gaa aaa atc aag gtt ggt gat gta gta gaa 967
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 135 140 145

gta cag gca gat gaa acc ttt ccc tgt gat ctt att ctt cta tca tct 1015
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tgc acc act gat gga acc tgt tat gtc act aca gcc agt ctt gat ggg 1063
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 165 170 175 180

gaa tcc aat tgc aag aca cat tat gca gta cgt gat acc att gca ctg 1111
 Glu Ser Asn Cys Lys Thr His Tyr Ala Val Arg Asp Thr Ile Ala Leu
 185 190 195

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 Cys Thr Ala Glu Ser Ile Asp Thr Leu Arg Ala Ala Ile Glu Cys Glu
 200 205 210

cag cct caa cct gac ctc tac aaa ttt gtt ggg cga atc aat atc tac 1207
 Gln Pro Gln Pro Asp Leu Tyr Lys Phe Val Gly Arg Ile Asn Ile Tyr
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 230 235 240

ttg ctg aaa gga gct acg cta aaa aat acc gag aag ata tat gga gtt 1303
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 245 250 255 260

gct gtt tac act gga atg gaa acc aaa atg gct ttg aac tac caa ggg 1351
 Ala Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu Asn Tyr Gln Gly
 265 270 275

aaa tct cag aaa cgt tct gct gtt gaa aaa tct att aat gct ttc ctg 1399
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 280 285 290

10046240
 10046240

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 295 300 305

cta aag tat gtt tgg caa agt acc cca tac aat gat gaa cct tgg tat 1495
 Leu Lys Tyr Val Trp Gln Ser Thr Pro Tyr Asn Asp Glu Pro Trp Tyr
 310 315 320

aac caa aag act cag aaa gag cga gag acc ttg aag gtt tta aaa atg 1543
 Asn Gln Lys Thr Gln Lys Glu Arg Glu Thr Leu Lys Val Leu Lys Met
 325 330 335 340

ttc acc gac ttc cta tca ttt atg gtt cta ttc aac ttt atc att cct 1591
 Phe Thr Asp Phe Leu Ser Phe Met Val Leu Phe Asn Phe Ile Ile Pro
 345 350 355

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 Val Ser Met Tyr Val Thr Val Glu Met Gln Lys Phe Leu Gly Ser Phe
 360 365 370

ttc atc tca tgg gat aag gac ttt tat gat gaa gaa att aat gaa gga 1687
 Phe Ile Ser Trp Asp Lys Asp Phe Tyr Asp Glu Glu Ile Asn Glu Gly
 375 380 385

gcc ctg gtt aac aca tca gac ctt aat gaa gaa ctt ggt cag gtg gat 1735
 Ala Leu Val Asn Thr Ser Asp Leu Asn Glu Glu Leu Gly Gln Val Asp
 390 395 400

tat gta ttt aca gat aag act gga aca ctc act gaa aac agc atg gaa 1783
 Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu Asn Ser Met Glu
 405 410 415 420

ttc att gaa tgc tgc ata gat ggc cac aaa tat aaa ggt gta act caa 1831
 Phe Ile Glu Cys Cys Ile Asp Gly His Lys Tyr Lys Gly Val Thr Gln
 425 430 435

gag gtt gat gga tta tct caa act gat gga act tta aca tat ttt gac 1879
 Glu Val Asp Gly Leu Ser Gln Thr Asp Gly Thr Leu Thr Tyr Phe Asp
 440 445 450

aaa gta gat aag aat cga gaa gag ctg ttt cta cgt gcc ttg tgt tta 1927
 Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg Ala Leu Cys Leu
 455 460 465

tgt cat act gta gaa atc aaa aca aac gat gct gtt gat gga gct aca 1975
 Cys His Thr Val Glu Ile Lys Thr Asn Asp Ala Val Asp Gly Ala Thr
 470 475 480

gaa tca gct gaa tta acc tat atc tcc tct tca cca gat gaa ata gct 2023
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 485 490 495 500

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 520 525 530

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 535 540 545
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 565 570 575 580
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 Thr Lys Val His Val Glu Arg Asn Ala Met Asp Gly Tyr Arg Thr Leu
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 Cys Val Ala Phe Lys Glu Ile Ala Pro Asp Asp Tyr Glu Arg Ile Asn
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 Glu Ala Leu His Ala Ala Gly Leu Lys Val Trp Val Leu Thr Gly Asp
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 Lys Met Glu Thr Ala Lys Ser Thr Cys Tyr Ala Cys Arg Leu Phe Gln
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 695 700 705
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 Glu Arg Lys Glu Asp Arg Leu His Glu Leu Leu Ile Glu Tyr Arg Lys
 710 715 720
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 Lys Leu Leu His Glu Phe Pro Lys Ser Thr Arg Ser Phe Lys Lys Ala
 725 730 735 740
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 745 750 755
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Leu Lys Gly Ser Pro Ile Thr Leu Ser Ile Gly Asp Gly Ala Asn Asp			
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gtt agt atg atc ttg gaa tcc cat gtg gga ata ggt att aaa ggc aaa			3031
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	840	845	850
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Lys His Leu Lys Lys Leu Leu Leu Ala His Gly His Leu Tyr Tyr Val			
	855	860	865
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Arg Ile Ala His Leu Val Gln Tyr Phe Phe Tyr Lys Asn Leu Cys Phe			
	870	875	880
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Ile Leu Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly Phe Ser Gln Gln			
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Pro Leu Tyr Asp Ala Ala Tyr Leu Thr Met Tyr Asn Ile Cys Phe Thr			
	905	910	915
tcc ttg ccc atc ctg gcc tat agt cta ctg gaa cag cac atc aac att			3319
Ser Leu Pro Ile Leu Ala Tyr Ser Leu Leu Glu Gln His Ile Asn Ile			
	920	925	930
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Asp Thr Leu Thr Ser Asp Pro Arg Leu Tyr Met Lys Ile Ser Gly Asn			
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gcc atg cta cag ttg ggc ccc ttc tta tat tgg aca ttt ctg gct gcc			3415
Ala Met Leu Gln Leu Gly Pro Phe Leu Tyr Trp Thr Phe Leu Ala Ala			
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ttt gaa ggg aca gtg ttc ttc ttt ggg act tac ttt ctt ttt cag act			3463
Phe Glu Gly Thr Val Phe Phe Phe Gly Thr Tyr Phe Leu Phe Gln Thr			
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Ala Ser Leu Glu Glu Asn Gly Lys Val Tyr Gly Asn Trp Thr Phe Gly			
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acc att gtt ttt aca gtc tta gta ttc act gta acc ctg aag ctt gcc			3559
Thr Ile Val Phe Thr Val Leu Val Phe Thr Val Thr Leu Lys Leu Ala			
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T0242001


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<212> PRT

<213> Homo sapiens

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Lys Tyr Thr Leu Trp Asn Phe Leu Pro Lys Asn Leu Phe Glu Gln Phe
50     55     60
Arg Arg Ile Ala Asn Phe Tyr Phe Leu Ile Ile Phe Leu Val Gln Val
65     70     75     80
Thr Val Asp Thr Pro Thr Ser Pro Val Thr Ser Gly Leu Pro Leu Phe
85     90     95
Phe Val Ile Thr Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu
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Arg His Arg Ala Asp Asn Glu Val Asn Lys Ser Thr Val Tyr Ile Ile
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Glu Asn Ala Lys Arg Val Arg Lys Glu Ser Glu Lys Ile Lys Val Gly
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Asp Val Val Glu Val Gln Ala Asp Glu Thr Phe Pro Cys Asp Leu Ile
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Ser Leu Asp Gly Glu Ser Asn Cys Lys Thr His Tyr Ala Val Arg Asp
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Thr Ile Ala Leu Cys Thr Ala Glu Ser Ile Asp Thr Leu Arg Ala Ala
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Ile Glu Cys Glu Gln Pro Gln Pro Asp Leu Tyr Lys Phe Val Gly Arg
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225    230    235    240
Pro Glu Asn Leu Leu Leu Lys Gly Ala Thr Leu Lys Asn Thr Glu Lys
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Ile Tyr Gly Val Ala Val Tyr Thr Gly Met Glu Thr Lys Met Ala Leu
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Asn Tyr Gln Gly Lys Ser Gln Lys Arg Ser Ala Val Glu Lys Ser Ile
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Asn Ala Phe Leu Ile Val Tyr Leu Phe Ile Leu Leu Thr Lys Ala Ala
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Val Cys Thr Thr Leu Lys Tyr Val Trp Gln Ser Thr Pro Tyr Asn Asp
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Glu Pro Trp Tyr Asn Gln Lys Thr Gln Lys Glu Arg Glu Thr Leu Lys
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102421 112920

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 Leu Gly Ser Phe Phe Ile Ser Trp Asp Lys Asp Phe Tyr Asp Glu Glu
 370 375 380
 Ile Asn Glu Gly Ala Leu Val Asn Thr Ser Asp Leu Asn Glu Glu Leu
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 Gly Gln Val Asp Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu
 405 410 415
 Asn Ser Met Glu Phe Ile Glu Cys Cys Ile Asp Gly His Lys Tyr Lys
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 Gly Val Thr Gln Glu Val Asp Gly Leu Ser Gln Thr Asp Gly Thr Leu
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 Thr Tyr Phe Asp Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg
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 Phe Lys Lys Ala Trp Thr Glu His Gln Glu Tyr Gly Leu Ile Ile Asp
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 785 790 795 800
 Met Val Lys Asn Leu Lys Gly Ser Pro Ile Thr Leu Ser Ile Gly Asp
 805 810 815
 Gly Ala Asn Asp Val Ser Met Ile Leu Glu Ser His Val Gly Ile Gly

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 Ile Lys Gly Lys Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp Tyr Ser
 835 840 845
 Val Pro Lys Phe Lys His Leu Lys Lys Leu Leu Leu Ala His Gly His
 850 855 860
 Leu Tyr Tyr Val Arg Ile Ala His Leu Val Gln Tyr Phe Phe Tyr Lys
 865 870 875 880
 Asn Leu Cys Phe Ile Leu Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly
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 995 1000 1005
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 Glu Ala Tyr Ile Ala Gln Arg Phe Cys Asp Asn Arg Ile Val Ser Ser

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Lys Tyr Thr Leu Trp Asn Phe Leu Pro Lys Asn Leu Phe Glu Gln Phe			
50	55	60	
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Phe Val Ile Thr Val Thr Ala Ile Lys Gln Gly Tyr Glu Asp Trp Leu			
100	105	110	
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Pro Glu Asn Leu Leu Leu Lys Gly Ala Thr Leu Lys Asn Thr Glu Lys			
245	250	255	
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Gly Gln Val Asp Tyr Val Phe Thr Asp Lys Thr Gly Thr Leu Thr Glu	
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Thr Tyr Phe Asp Lys Val Asp Lys Asn Arg Glu Glu Leu Phe Leu Arg	
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Leu Gly Asn Arg Asn Gly Tyr Met Arg Val Glu Asn Gln Arg Lys Glu	
515 520 525	

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Tyr Arg Thr Leu Cys Val Ala Phe Lys Glu Ile Ala Pro Asp Asp Tyr	
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Phe Ala Gln Met Leu Ser Ser Val Ser Thr Trp Leu Ala Ile Ile Leu
1060      1065      1070

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Met Thr Glu Ala Leu Gln Trp
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25 30 35

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Ser Ser Gln Ile Pro Lys Leu Ser Gly Arg His Arg Ile Val Val Pro
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1010
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His	Glu	Thr	Lys	Ala	Met	Leu	Asn	Asn	Ser	Gly	Pro	Arg	Tyr	Lys	Arg		
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Ser	Lys	Leu	Glu	Arg	Arg	Ala	Asn	Thr	Asp	Val	Leu	Trp	Cys	Val	Met		
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ctt	ctg	gtc	ata	atg	tgc	tta	act	ggc	gca	gta	ggg	cat	gga	atc	tgg	1301	
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Ile	Glu	Ile	Val	Lys	Leu	Gly	Gln	Ile	Tyr	Phe	Ile	Gln	Ser	Asp	Val		
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Asp	Phe	Tyr	Asn	Glu	Lys	Met	Asp	Ser	Ile	Val	Gln	Cys	Arg	Ala	Leu		
		410					415					420					
aac	atc	gcc	gag	gat	ctg	gga	cag	att	cag	tac	ctc	ttt	tcc	gat	aag	1589	
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TO THE "EAGLE"

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Ser Ala Cys Cys Thr Glu Thr Glu Lys Gln His Gly Asp Ala Gly Leu	
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Ser Asp Thr Arg Thr Ile Tyr Val Ala His Arg Phe Pro Gln Asn Gly	
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Leu Tyr Thr Pro Gln Lys Phe Ile Asp Asn Arg Ile Ile Ser Ser Lys	
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Variable	Mean	SD	Min	Max
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Gender	1.2	0.4	1	2
Marital status	1.5	0.5	1	3
Education	12.5	2.5	9	16
Occupation	1.8	0.8	1	3
Income	1.5	0.5	1	3
Health status	1.2	0.4	1	2
Stress level	1.8	0.8	1	3
Life satisfaction	1.5	0.5	1	3
Depression	1.2	0.4	1	2
Anxiety	1.5	0.5	1	3
Loneliness	1.8	0.8	1	3
Self-esteem	1.5	0.5	1	3
Resilience	1.2	0.4	1	2
Optimism	1.5	0.5	1	3
Gratitude	1.8	0.8	1	3
Forgiveness	1.5	0.5	1	3
Compassion	1.2	0.4	1	2
Empathy	1.5	0.5	1	3
Kindness	1.8	0.8	1	3
Generosity	1.5	0.5	1	3
Patience	1.2	0.4	1	2
Humility	1.5	0.5	1	3
Modesty	1.8	0.8	1	3
Shame	1.5	0.5	1	3
Guilt	1.2	0.4	1	2
Envy	1.5	0.5	1	3
Jealousy	1.8	0.8	1	3
Anger	1.5	0.5	1	3
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Disagreeing	1.8	0.8	1	3
Disrespecting	1.5	0.5	1	3
Disapprovingly	1.2	0.4	1	2
Disagreeingly	1.5	0.5	1	3
Disrespectfully	1.8	0.8	1	3
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 Trp Tyr Arg Asn Leu Phe Arg Phe Leu Leu Leu Phe Ser Tyr Ile Ile
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 His Val Arg Asp Ser Tyr Ser Gln Met Gln Ser Gln Ala Gly Gly Asn
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Ile	His	Ile	Phe	Arg	Gln	Val	Thr	Ser	Arg	Gly	Glu	Ala	His	Leu	Glu		
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 Ser Ser Asp Ile Gln Val Gly Asp Leu Ile Ile Val Glu Lys Asn Gln
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 Arg Ile Pro Ser Asp Met Val Phe Leu Arg Thr Ser Glu Lys Ala Gly
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tcg tgt ttt att cga act gat caa cta gat ggt gaa act gac tgg aag 672
 Ser Cys Phe Ile Arg Thr Asp Gln Leu Asp Gly Glu Thr Asp Trp Lys
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att cac agt ttc gaa ggc aca ttt acc agg gaa gac agt gac ccg ccc 816
 Ile His Ser Phe Glu Gly Thr Phe Thr Arg Glu Asp Ser Asp Pro Pro
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 Thr Arg Ser Val Met Asn Thr Ser Asn Pro Lys Asn Lys Val Gly Leu
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 Trp Thr Glu Ser Val Gly Leu Thr Leu Val Ser Arg Asp Leu Thr Ser
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Gln Ala Lys Leu Ser Met His Asp Arg Ser Leu Lys Val Ala Ala Val	660	665	670	
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Val Glu Ser Leu Glu Arg Glu Met Glu Leu Leu Cys Leu Thr Gly Val	675	680	685	
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Asn Ala Gly Ile Lys Ile Trp Met Leu Thr Gly Asp Lys Leu Glu Thr	705	710	715	720
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Ala Thr Cys Ile Ala Lys Ser Ser His Leu Val Ser Arg Thr Gln Asp	725	730	735	
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Ile His Ile Phe Arg Gln Val Thr Ser Arg Gly Glu Ala His Leu Glu	740	745	750	
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Leu Asn Ala Phe Arg Arg Lys His Asp Cys Ala Leu Val Ile Ser Gly	755	760	765	
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Gln Lys Ala Arg Ile Val Thr Leu Leu Gln Gln His Thr Gly Arg Arg	805	810	815	
acc tgc gcc atc ggt gat gga gga aat gat gtc agc atg att cag gca				2496
Thr Cys Ala Ile Gly Asp Gly Gly Asn Asp Val Ser Met Ile Gln Ala	820	825	830	
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Ala Asp Cys Gly Ile Gly Ile Glu Gly Lys Glu Gly Lys Gln Ala Ser	835	840	845	
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Leu Ala Ala Asp Phe Ser Ile Thr Gln Phe Arg His Ile Gly Arg Leu	850	855	860	
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Leu Met Val His Gly Arg Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly	865	870	875	880

The "GAT" sequence

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 Leu Met Val Gly Tyr Ala Thr Ile Tyr Thr Met Phe Pro Val Phe Ser
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 Glu Leu Tyr Lys Asp Leu Thr Lys Gly Arg Ser Leu Ser Phe Lys Thr
 945 950 955 960
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                               Met Pro Leu Met Met Ser
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Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly Val Leu Tyr Glu Gln Phe
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Gly Asp Leu Ile Ile Val Glu Lys Asn Gln Arg Ile Pro Ser Asp Met
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00463-400

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Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu	Cys	Gly	Asn	Met	Ala	Arg		
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gaa	gga	ctg	cgg	acc	ctc	gtg	gtt	gca	aag	aag	gcg	ttg	aca	gag	gag	2093	
Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys	Lys	Ala	Leu	Thr	Glu	Glu		
				635					640					645			
cag	tac	cag	gac	ttt	gag	agc	cga	tac	act	caa	gcc	aag	ctg	agc	atg	2141	
Gln	Tyr	Gln	Asp	Phe	Glu	Ser	Arg	Tyr	Thr	Gln	Ala	Lys	Leu	Ser	Met		
			650					655					660				
cac	gac	agg	tcc	ctc	aag	gtg	gcc	gcg	gta	gtc	gag	agc	ctg	gag	agg	2189	
His	Asp	Arg	Ser	Leu	Lys	Val	Ala	Ala	Val	Val	Glu	Ser	Leu	Glu	Arg		
		665				670						675					
gag	atg	gaa	ctg	ctg	tgc	ctc	acc	ggc	gtg	gag	gac	cag	ctg	cag	gca	2237	
Glu	Met	Glu	Leu	Leu	Cys	Leu	Thr	Gly	Val	Glu	Asp	Gln	Leu	Gln	Ala		
	680					685					690						
gac	gtg	cgg	ccc	acg	ctg	gag	atg	ctg	cgc	aac	gcc	ggg	atc	aag	ata	2285	
Asp	Val	Arg	Pro	Thr	Leu	Glu	Met	Leu	Arg	Asn	Ala	Gly	Ile	Lys	Ile		

T04463007

695	700	705	710	
tgg atg cta aca ggc gat aaa ctc gag aca gct acc tgc att gcc aaa				2333
Trp Met Leu Thr Gly Asp Lys Leu Glu Thr Ala Thr Cys Ile Ala Lys	715	720	725	
agt tca cat ctc gtg tct aga aca caa gat att cat att ttc aga cag				2381
Ser Ser His Leu Val Ser Arg Thr Gln Asp Ile His Ile Phe Arg Gln	730	735	740	
gta acc agt cgg gga gag gca cat ttg gag ctg aat gca ttt cga agg				2429
Val Thr Ser Arg Gly Glu Ala His Leu Glu Leu Asn Ala Phe Arg Arg	745	750	755	
aag cat gat tgt gca cta gtc ata tct ggg gac tct ctg gag gtt tgt				2477
Lys His Asp Cys Ala Leu Val Ile Ser Gly Asp Ser Leu Glu Val Cys	760	765	770	
cta aag tac tac gag cat gaa ttt gtg gag ctg gcc tgc cag tgc cct				2525
Leu Lys Tyr Tyr Glu His Glu Phe Val Glu Leu Ala Cys Gln Cys Pro	775	780	785	790
gcc gtg gtt tgc tgc cgc tgc tca ccc acc cag aag gcc cgc att gtg				2573
Ala Val Val Cys Cys Arg Cys Ser Pro Thr Gln Lys Ala Arg Ile Val	795	800	805	
aca ctg ctg cag cag cac aca ggg aga cgc acc tgc gcc atc ggt gat				2621
Thr Leu Leu Gln Gln His Thr Gly Arg Arg Thr Cys Ala Ile Gly Asp	810	815	820	
gga gga aat gat gtc agc atg att cag gca gca gac tgt ggg att ggg				2669
Gly Gly Asn Asp Val Ser Met Ile Gln Ala Ala Asp Cys Gly Ile Gly	825	830	835	
att gag gga aag gag ggt aaa cag gcc tcg ctg gcg gcc gac ttc tcc				2717
Ile Glu Gly Lys Glu Gly Lys Gln Ala Ser Leu Ala Ala Asp Phe Ser	840	845	850	
atc acg cag ttc cgg cac ata ggc agg ctg ctc atg gtg cac ggg cgg				2765
Ile Thr Gln Phe Arg His Ile Gly Arg Leu Leu Met Val His Gly Arg	855	860	865	870
aac agc tac aag agg tcg gcg gca ctc ggc cag ttc gtc atg cac agg				2813
Asn Ser Tyr Lys Arg Ser Ala Ala Leu Gly Gln Phe Val Met His Arg	875	880	885	
ggc ctt atc atc tcc acc atg cag gct gtg ttt tcc tca gtc ttc tac				2861
Gly Leu Ile Ile Ser Thr Met Gln Ala Val Phe Ser Ser Val Phe Tyr	890	895	900	
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Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe Leu Met Val Gly Tyr Ala	905	910	915	
acc ata tac acc atg ttc cca gtg ttc tcc tta gtg ctg gac cag gac				2957
Thr Ile Tyr Thr Met Phe Pro Val Phe Ser Leu Val Leu Asp Gln Asp	920	925	930	
gtg aag cca gag atg gcg atg ctc tac ccg gag ctg tac aag gac ctc				3005
Val Lys Pro Glu Met Ala Met Leu Tyr Pro Glu Leu Tyr Lys Asp Leu	935	940	945	950

100463662001

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Asn	Arg	Thr	Tyr	Gln	Ala	Ser	Ser	Pro	Asp	Glu	Val	Ala	Leu	Val	Gln
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Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Thr	Ser
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Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Ser	Phe	Cys	Ile	Leu
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Gln	Leu	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Val	Ile	Val
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Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp
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Val	Ala	Met	Ser	Pro	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu
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Cys	Gly	Asn	Met	Ala	Arg	Glu	Gly	Leu	Arg	Thr	Leu	Val	Val	Ala	Lys
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Lys	Ala	Leu	Thr	Glu	Glu	Gln	Tyr	Gln	Asp	Phe	Glu	Ser	Arg	Tyr	Thr
			645						650					655	
Gln	Ala	Lys	Leu	Ser	Met	His	Asp	Arg	Ser	Leu	Lys	Val	Ala	Ala	Val
			660					665					670		
Val	Glu	Ser	Leu	Glu	Arg	Glu	Met	Glu	Leu	Leu	Cys	Leu	Thr	Gly	Val
		675					680						685		
Glu	Asp	Gln	Leu	Gln	Ala	Asp	Val	Arg	Pro	Thr	Leu	Glu	Met	Leu	Arg
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Asn	Ala	Gly	Ile	Lys	Ile	Trp	Met	Leu	Thr	Gly	Asp	Lys	Leu	Glu	Thr
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Ala	Thr	Cys	Ile	Ala	Lys	Ser	Ser	His	Leu	Val	Ser	Arg	Thr	Gln	Asp
			725						730					735	
Ile	His	Ile	Phe	Arg	Gln	Val	Thr	Ser	Arg	Gly	Glu	Ala	His	Leu	Glu
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Asp	Ser	Leu	Glu	Val	Cys	Leu	Lys	Tyr	Tyr	Glu	His	Glu	Phe	Val	Glu
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Gln	Lys	Ala	Arg	Ile	Val	Thr	Leu	Leu	Gln	Gln	His	Thr	Gly	Arg	Arg
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Thr	Cys	Ala	Ile	Gly	Asp	Gly	Gly	Asn	Asp	Val	Ser	Met	Ile	Gln	Ala
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Ala	Asp	Cys	Gly	Ile	Gly	Ile	Glu	Gly	Lys	Glu	Gly	Lys	Gln	Ala	Ser
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Leu	Ala	Ala	Asp	Phe	Ser	Ile	Thr	Gln	Phe	Arg	His	Ile	Gly	Arg	Leu
		850					855					860			
Leu	Met	Val	His	Gly	Arg	Asn	Ser	Tyr	Lys	Arg	Ser	Ala	Ala	Leu	Gly
865					870					875					880
Gln	Phe	Val	Met	His	Arg	Gly	Leu	Ile	Ile	Ser	Thr	Met	Gln	Ala	Val
			885						890					895	
Phe	Ser	Ser	Val	Phe	Tyr	Phe	Ala	Ser	Val	Pro	Leu	Tyr	Gln	Gly	Phe
			900					905					910		
Leu	Met	Val	Gly	Tyr	Ala	Thr	Ile	Tyr	Thr	Met	Phe	Pro	Val	Phe	Ser
		915					920						925		
Leu	Val	Leu	Asp	Gln	Asp	Val	Lys	Pro	Glu	Met	Ala	Met	Leu	Tyr	Pro
		930					935					940			
Glu	Leu	Tyr	Lys	Asp	Leu	Thr	Lys	Gly	Arg	Ser	Leu	Ser	Phe	Lys	Thr
945					950					955					960
Phe	Leu	Ile	Trp	Val	Leu	Ile	Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Leu	Met
			965						970					975	

100433-100434

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 980 985 990
 Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Met Val Ala Leu
 995 1000 1005
 Thr Val Arg Thr Trp His Trp Leu Met Val Val Ala Glu Phe Leu Ser
 1010 1015 1020
 Leu Gly Cys Tyr Val Ser Ser Leu Ala Phe Leu Asn Glu Tyr Phe Gly
 1025 1030 1035 1040
 Ile Gly Arg Val Ser Phe Gly Ala Phe Leu Asp Val Ala Phe Ile Thr
 1045 1050 1055
 Thr Val Thr Phe Leu Trp Lys Val Ser Ala Ile Thr Val Val Ser Cys
 1060 1065 1070
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 1075 1080 1085
 Ser Tyr Cys Lys Leu Ala Ser
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 tac cac acc tta cca cga gcc agg ata atg caa agg aaa aga gga ctg 96
 Tyr His Thr Leu Pro Arg Ala Arg Ile Met Gln Arg Lys Arg Gly Leu
 20 25 30
 gag tgg ttt gtc tgt gat ggc tgg aag ttc ctc tgt acc agt tgc tgt 144
 Glu Trp Phe Val Cys Asp Gly Trp Lys Phe Leu Cys Thr Ser Cys Cys
 35 40 45
 ggt tgg ctg ata aat att tgt cga aga aag aaa gag ctg aaa gct cgc 192
 Gly Trp Leu Ile Asn Ile Cys Arg Arg Lys Lys Glu Leu Lys Ala Arg
 50 55 60
 aca gta tgg ctt gga tgt cct gaa aag tgt gaa gaa aaa cat ccc agg 240
 Thr Val Trp Leu Gly Cys Pro Glu Lys Cys Glu Glu Lys His Pro Arg
 65 70 75 80
 aat tct ata aaa aat caa aaa tac aat gtg ttt acc ttt ata cct ggg 288
 Asn Ser Ile Lys Asn Gln Lys Tyr Asn Val Phe Thr Phe Ile Pro Gly
 85 90 95
 gtt ttg tat gaa caa ttc aag ttt ttc ttg aat ctc tat ttt cta gtg 336
 Val Leu Tyr Glu Gln Phe Lys Phe Phe Leu Asn Leu Tyr Phe Leu Val
 100 105 110
 ata tcc tgc tca cag ttt gta cca gca ttg aaa ata ggc tat ctc tac 384
 Ile Ser Cys Ser Gln Phe Val Pro Ala Leu Lys Ile Gly Tyr Leu Tyr
 115 120 125
 acc tac tgg gct cct ctg gga ttt gtc ttg gct gtt act atg aca cgg 432

Thr	Tyr	Trp	Ala	Pro	Leu	Gly	Phe	Val	Leu	Ala	Val	Thr	Met	Thr	Arg	
130						135					140					
gaa	gca	att	gat	gaa	ttt	cgg	cgt	ttt	cag	cgt	gac	aag	gaa	gtg	aat	480
Glu	Ala	Ile	Asp	Glu	Phe	Arg	Arg	Phe	Gln	Arg	Asp	Lys	Glu	Val	Asn	
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tca	caa	cta	tat	agc	aag	ctt	aca	gta	aga	ggt	aaa	gtg	caa	gtt	aag	528
Ser	Gln	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Arg	Gly	Lys	Val	Gln	Val	Lys	
				165					170					175		
agt	tca	gac	ata	caa	gtt	gga	gac	ctc	atc	ata	gtg	gaa	aag	aat	caa	576
Ser	Ser	Asp	Ile	Gln	Val	Gly	Asp	Leu	Ile	Ile	Val	Glu	Lys	Asn	Gln	
			180					185					190			
aga	att	cca	tcg	gac	atg	gtg	ttt	ctt	agg	act	tca	gaa	aaa	gca	ggt	624
Arg	Ile	Pro	Ser	Asp	Met	Val	Phe	Leu	Arg	Thr	Ser	Glu	Lys	Ala	Gly	
		195					200					205				
tcg	tgt	ttt	att	cga	act	gat	caa	cta	gat	ggt	gaa	act	gac	tgg	aag	672
Ser	Cys	Phe	Ile	Arg	Thr	Asp	Gln	Leu	Asp	Gly	Glu	Thr	Asp	Trp	Lys	
	210					215					220					
ctg	aag	gtg	gca	gtg	agc	tgc	acg	caa	cag	ctg	ccg	gct	ctg	ggg	gac	720
Leu	Lys	Val	Ala	Val	Ser	Cys	Thr	Gln	Gln	Leu	Pro	Ala	Leu	Gly	Asp	
225					230					235					240	
ctt	ttt	tct	atc	agt	gct	tat	gtt	tat	gct	cag	aaa	cca	caa	atg	gac	768
Leu	Phe	Ser	Ile	Ser	Ala	Tyr	Val	Tyr	Ala	Gln	Lys	Pro	Gln	Met	Asp	
				245					250					255		
att	cac	agt	ttc	gaa	ggc	aca	ttt	acc	agg	gaa	gac	agt	gac	ccg	ccc	816
Ile	His	Ser	Phe	Glu	Gly	Thr	Phe	Thr	Arg	Glu	Asp	Ser	Asp	Pro	Pro	
			260					265					270			
att	cat	gaa	agt	ctc	agc	ata	gaa	aat	aca	ttg	tgg	gca	agc	acc	att	864
Ile	His	Glu	Ser	Leu	Ser	Ile	Glu	Asn	Thr	Leu	Trp	Ala	Ser	Thr	Ile	
		275					280					285				
gtt	gca	tca	ggt	act	gta	ata	ggt	gtt	gtc	att	tat	acc	gga	aaa	gag	912
Val	Ala	Ser	Gly	Thr	Val	Ile	Gly	Val	Val	Ile	Tyr	Thr	Gly	Lys	Glu	
	290					295					300					
act	cga	agt	gta	atg	aac	aca	tcc	aat	cca	aaa	aat	aag	gtt	ggt	ttg	960
Thr	Arg	Ser	Val	Met	Asn	Thr	Ser	Asn	Pro	Lys	Asn	Lys	Val	Gly	Leu	
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ttg	gac	ctt	gaa	ctc	aat	cgg	ctg	acg	aaa	gcg	cta	ttt	ttg	gct	tta	1008
Leu	Asp	Leu	Glu	Leu	Asn	Arg	Leu	Thr	Lys	Ala	Leu	Phe	Leu	Ala	Leu	
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Val	Ala	Leu	Ser	Ile	Val	Met	Val	Thr	Leu	Gln	Gly	Phe	Val	Gly	Pro	
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tgg	tac	cgc	aat	ctt	ttt	cgg	ttc	ctt	ctc	ctc	ttt	tct	tac	atc	att	1104
Trp	Tyr	Arg	Asn	Leu	Phe	Arg	Phe	Leu	Leu	Leu	Phe	Ser	Tyr	Ile	Ile	
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ccc	ata	agt	ttg	cgt	gtg	aac	ttg	gac	atg	ggc	aaa	gcg	gtg	tat	gga	1152
Pro	Ile	Ser	Leu	Arg	Val	Asn	Leu	Asp	Met	Gly	Lys	Ala	Val	Tyr	Gly	

TOGETHER

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Trp Met Met Met Lys Asp Glu Asn Ile Pro Gly Thr Val Val Arg Thr			
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agc act atc cca gag gaa ctt ggg cgc ctg gtg tat tta ttg aca gac			1248
Ser Thr Ile Pro Glu Glu Leu Gly Arg Leu Val Tyr Leu Leu Thr Asp			
405	410		415
aaa aca gga acc ctc acc cag aat gaa atg ata ttt aag cgg ctg cac			1296
Lys Thr Gly Thr Leu Thr Gln Asn Glu Met Ile Phe Lys Arg Leu His			
420	425		430
ctg ggc acc gtg tcc tat ggc gcc gac acg atg gat gag atc cag agc			1344
Leu Gly Thr Val Ser Tyr Gly Ala Asp Thr Met Asp Glu Ile Gln Ser			
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cat gtc agg gac tcc tac tca cag atg cag tct caa gct ggt gga aac			1392
His Val Arg Asp Ser Tyr Ser Gln Met Gln Ser Gln Ala Gly Gly Asn			
450	455		460
aat act ggt tca act cca cta aga aaa gcc caa tct tca gct ccc aaa			1440
Asn Thr Gly Ser Thr Pro Leu Arg Lys Ala Gln Ser Ser Ala Pro Lys			
465	470		480
gtt agg aaa agt gtc agt agt cga atc cat gaa gcc gtg aaa gcc atc			1488
Val Arg Lys Ser Val Ser Ser Arg Ile His Glu Ala Val Lys Ala Ile			
485	490		495
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Val Leu Cys His Asn Val Thr Pro Val Tyr Glu Ser Arg Ala Gly Val			
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act gag gag act gag ttc gca gag gct gac caa gac ttc agt gat gag			1584
Thr Glu Glu Thr Glu Phe Ala Glu Ala Asp Gln Asp Phe Ser Asp Glu			
515	520		525
aat cgc acc tac cag gct tcc agc ccg gat gag gtc gct ctg gtg cag			1632
Asn Arg Thr Tyr Gln Ala Ser Ser Pro Asp Glu Val Ala Leu Val Gln			
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Trp Thr Glu Ser Val Gly Leu Thr Leu Val Ser Arg Asp Leu Thr Ser			
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Met Gln Leu Lys Thr Pro Ser Gly Gln Val Leu Ser Phe Cys Ile Leu			
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Gln Leu Phe Pro Phe Thr Ser Glu Ser Lys Arg Met Gly Val Ile Val			
580	585		590
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Arg Asp Glu Ser Thr Ala Glu Ile Thr Phe Tyr Met Lys Gly Ala Asp			
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Val Ala Met Ser Pro Ile Val Gln Tyr Asn Asp Trp Leu Glu Glu Glu			
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The "cag" code

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 cag ttc gtc atg cac agg ggc ctt atc atc tcc acc atg cag gct gtg 2688
 Gln Phe Val Met His Arg Gly Leu Ile Ile Ser Thr Met Gln Ala Val
 885 890 895
 ttt tcc tca gtc ttc tac ttc gca tcc gtc cct ttg tat cag ggc ttc 2736
 Phe Ser Ser Val Phe Tyr Phe Ala Ser Val Pro Leu Tyr Gln Gly Phe
 900 905 910
 ctc atg gtg ggg tat gcc acc ata tac acc atg ttc cca gtg ttc tcc 2784
 Leu Met Val Gly Tyr Ala Thr Ile Tyr Thr Met Phe Pro Val Phe Ser
 915 920 925
 tta gtg ctg gac cag gac gtg aag cca gag atg gcg atg ctc tac ccg 2832
 Leu Val Leu Asp Gln Asp Val Lys Pro Glu Met Ala Met Leu Tyr Pro
 930 935 940
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 Glu Leu Tyr Lys Asp Leu Thr Lys Gly Arg Ser Leu Ser Phe Lys Thr
 945 950 955 960
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 Phe Leu Ile Trp Val Leu Ile Ser Ile Tyr Gln Gly Gly Ile Leu Met
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 Tyr Gly Ala Leu Val Leu Phe Glu Ser Glu Phe Val His Val Val Ala
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 Ile Ser Phe Thr Ala Leu Ile Leu Thr Glu Leu Leu Met Val Ala Leu
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 1075 1080

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<212> PRT

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 Ser Val Val Gly Thr Gly Leu Phe Leu Pro Pro Leu Gln Leu Leu Leu
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 Pro Pro Arg Leu Leu Phe Thr His Ala Ile Leu Glu Arg Leu His Leu
 85 90 95
 Trp Leu Ala Leu Pro Pro Val Leu Val Leu Gly His Ala Leu Leu His
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 Cys Lys Val Gly Gly Ser Thr Ala Arg Ala Gly Asp Gln Leu Val Gln
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 Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val Leu Gln Ala Ile
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 Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu Val Met Lys Gly
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 Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser Leu Lys Asp Glu
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<210> 32

<211> 1237

<212> PRT

<213> Rattus norvegicus

<400> 32

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Gln Val Ile Val Ala Thr Ile Ser Phe Leu Glu Thr Met Leu Leu Ile
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Phe Val Leu Glu Met Ile Asn Thr Leu Pro Phe Ile Ile Thr Val Phe
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 <211> 638
 <212> PRT
 <213> Rattus norvegicus

<400> 33

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TOP SECRET

Protein Data Bank

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<211> 1187

<212> PRT

<213> Mus musculus

<400> 34

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Arg Ile Val Ser Ser Lys	Tyr Thr Phe Trp Asn	Phe Ile Pro Lys Asn
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Leu Phe Glu Gln Phe Arg	Arg Ile Ala Asn Phe	Tyr Phe Leu Ile Ile
65	70	75
Phe Leu Val Gln Leu Ile	Ile Asp Thr Pro Thr	Ser Pro Val Thr Ser
85	90	95
Gly Leu Pro Leu Phe Phe	Val Ile Thr Val Thr	Ala Ile Lys Gln Gly
100	105	110
Tyr Glu Asp Trp Leu Arg	His Lys Ala Asp Asn	Ala Met Asn Gln Cys
115	120	125
Pro Val His Phe Ile Gln	His Gly Lys Leu Val	Arg Lys Gln Ser Arg
130	135	140
Lys Leu Arg Val Gly Asp	Ile Val Met Val Lys	Glu Asp Glu Thr Phe
145	150	155
Pro Cys Asp Leu Ile Phe	Leu Ser Ser Asn Arg	Ala Asp Gly Thr Cys
165	170	175
His Val Thr Thr Ala Ser	Leu Asp Gly Glu Ser	Ser His Lys Thr His
180	185	190
Tyr Ala Val Gln Asp Thr	Lys Gly Phe His Thr	Glu Ala Asp Val Asp
195	200	205
Ser Leu His Ala Thr Ile	Glu Cys Glu Gln Pro	Gln Pro Asp Leu Tyr
210	215	220

Lys Phe Val Gly Arg Ile Asn Val Tyr Asn Asp Leu Asn Asp Pro Val
 225 230 235 240
 Val Arg Pro Leu Gly Ser Glu Asn Leu Leu Arg Gly Ala Thr Leu
 245 250 255
 Lys Asn Thr Glu Lys Ile Phe Gly Val Ala Ile Tyr Thr Gly Met Glu
 260 265 270
 Thr Lys Met Ala Leu Asn Tyr Gln Ser Lys Ser Gln Lys Arg Ser Ala
 275 280 285
 Val Glu Lys Ser Met Asn Thr Phe Leu Ile Val Tyr Leu Cys Ile Leu
 290 295 300
 Val Ser Lys Ala Leu Ile Asn Thr Val Leu Lys Tyr Val Trp Gln Ser
 305 310 315 320
 Glu Pro Phe Arg Asp Glu Pro Trp Tyr Asn Glu Lys Thr Glu Ser Glu
 325 330 335
 Arg Gln Arg Asn Leu Phe Leu Arg Ala Phe Thr Asp Phe Leu Ala Phe
 340 345 350
 Met Val Leu Phe Asn Tyr Ile Ile Pro Val Ser Met Tyr Val Thr Val
 355 360 365
 Glu Met Gln Lys Phe Leu Gly Ser Tyr Phe Ile Thr Trp Asp Glu Asp
 370 375 380
 Met Phe Asp Glu Glu Met Gly Glu Gly Pro Leu Val Asn Thr Ser Asp
 385 390 395 400
 Leu Asn Glu Glu Leu Gly Gln Val Glu Tyr Ile Phe Thr Asp Lys Thr
 405 410 415
 Gly Thr Leu Thr Glu Asn Asn Met Ala Phe Lys Glu Cys Cys Ile Glu
 420 425 430
 Gly His Val Tyr Val Pro His Val Ile Cys Asn Gly Gln Val Leu Pro
 435 440 445
 Asp Ser Ser Gly Ile Asp Met Ile Asp Ser Ser Pro Gly Val Cys Gly
 450 455 460
 Arg Glu Arg Glu Glu Leu Phe Phe Arg Ala Ile Cys Leu Cys His Thr
 465 470 475 480
 Val Gln Val Lys Asp Asp His Cys Gly Asp Asp Val Asp Gly Pro Gln
 485 490 495
 Lys Ser Pro Asp Ala Lys Ser Cys Val Tyr Ile Ser Ser Ser Pro Asp
 500 505 510
 Glu Val Ala Leu Val Glu Gly Val Gln Arg Leu Gly Phe Thr Tyr Leu
 515 520 525
 Arg Leu Lys Asp Asn Tyr Met Glu Ile Leu Asn Arg Glu Asn Asp Ile
 530 535 540
 Glu Arg Phe Glu Leu Leu Glu Val Leu Thr Phe Asp Ser Val Arg Arg
 545 550 555 560
 Arg Met Ser Val Ile Val Lys Ser Thr Thr Gly Glu Ile Tyr Leu Phe
 565 570 575
 Cys Lys Gly Ala Asp Ser Ser Ile Phe Pro Arg Val Ile Glu Gly Lys
 580 585 590
 Val Asp Gln Val Arg Ser Arg Val Glu Arg Asn Ala Val Glu Gly Leu
 595 600 605
 Arg Thr Leu Cys Val Ala Tyr Lys Arg Leu Glu Pro Glu Gln Tyr Glu
 610 615 620
 Asp Ala Cys Arg Leu Leu Gln Ser Ala Lys Val Ala Leu Gln Asp Arg
 625 630 635 640
 Glu Lys Lys Leu Ala Glu Ala Tyr Glu Gln Ile Glu Lys Asp Leu Val
 645 650 655
 Leu Leu Gly Ala Thr Ala Val Glu Asp Arg Leu Gln Glu Lys Ala Ala
 660 665 670
 Asp Thr Ile Glu Ala Leu Gln Lys Ala Gly Ile Lys Val Trp Val Leu
 675 680 685
 Thr Gly Asp Lys Met Glu Thr Ala Ser Ala Thr Cys Tyr Ala Cys Lys
 690 695 700
 Leu Phe Arg Arg Ser Thr Gln Leu Leu Glu Leu Thr Thr Lys Lys Leu

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705 710 715 720
 Glu Glu Gln Ser Leu His Asp Val Leu Phe Asp Leu Ser Lys Thr Val
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 Leu Arg Cys Ser Gly Ser Met Thr Arg Asp Ser Phe Ser Gly Leu Ser
 740 745 750
 Thr Asp Met His Asp Tyr Gly Leu Ile Ile Asp Gly Ala Ala Leu Ser
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 Leu Ile Met Lys Pro Arg Glu Asp Gly Ser Ser Ser Gly Asn Tyr Arg
 770 775 780
 Glu Leu Phe Leu Glu Ile Cys Arg Asn Cys Ser Ala Val Leu Cys Cys
 785 790 795 800
 Arg Met Ala Pro Leu Gln Lys Ala Gln Ile Val Lys Leu Ile Lys Phe
 805 810 815
 Ser Lys Glu His Pro Ile Thr Leu Ala Ile Gly Asp Gly Ala Asn Asp
 820 825 830
 Val Ser Met Ile Leu Glu Ala His Val Gly Ile Gly Val Ile Gly Lys
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 Glu Gly Arg Gln Ala Ala Arg Asn Ser Asp Tyr Ala Ile Pro Lys Phe
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 Lys His Leu Lys Lys Met Leu Leu Val His Gly His Phe Tyr Tyr Ile
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 Arg Ile Ser Glu Leu Val Gln Tyr Phe Phe Tyr Lys Asn Val Cys Phe
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 Ile Phe Pro Gln Phe Leu Tyr Gln Phe Phe Cys Gly Phe Ser Gln Gln
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 Thr Leu Tyr Asp Thr Ala Tyr Leu Thr Leu Tyr Asn Ile Ser Phe Thr
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 Ser Leu Pro Ile Leu Leu Tyr Ser Leu Met Glu Gln His Val Gly Ile
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 Asp Val Leu Lys Arg Asp Pro Thr Leu Tyr Arg Asp Ile Ala Lys Asn
 945 950 955 960
 Ala Leu Leu Arg Trp Arg Val Phe Ile Tyr Trp Thr Phe Leu Gly Val
 965 970 975
 Phe Asp Ala Leu Val Phe Phe Phe Gly Ala Tyr Phe Ile Phe Glu Asn
 980 985 990
 Thr Thr Val Thr Ile Asn Gly Gln Met Phe Gly Asn Trp Thr Phe Gly
 995 1000 1005
 Thr Leu Val Phe Thr Val Met Val Leu Thr Val Thr Leu Lys Leu Ala
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 Leu Asp Thr His Tyr Trp Thr Trp Ile Asn His Phe Val Ile Trp Gly
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 1140 1145 1150
 Cys Ser Arg Trp Glu Ser Glu Glu Cys Pro Val Leu Pro Leu His Pro
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 Met Pro Thr
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Ser	Gly	Ile	Glu	Tyr	Ser	His	Asp	Ala	Asn	Ala	Gln	Arg	Leu	Ala	Arg					
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Tyr	Gln	Glu	Ala	Asp	Ser	Glu	Glu	Glu	Glu	Val	Val	Ser	Lys	Val	Gly					
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Ser	Pro	Met	Glu	Lys	Asp	Ile	Thr	Pro	Asp	Pro	Lys	Leu	Leu	Glu	Lys					
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Pro	Leu	Ala	His	Leu	Ser	Pro	Glu	Leu	Ser	Asp	Val	Phe	Asp	Phe	Phe					
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Pro	Arg	Gln	Lys	Val	Arg	Val	Arg	Phe	Glu	Leu	Lys	Ser	Pro	Val	Lys					
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Leu	Asp	Leu	Glu	Leu	Asn	Gln	Leu	Thr	Lys	Ala	Leu	Phe	Leu	Ala	Leu
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Val	Val	Leu	Ser	Val	Val	Met	Val	Thr	Leu	Gln	Gly	Phe	Ala	Gly	Pro
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Trp	Tyr	Arg	Asn	Leu	Phe	Arg	Phe	Leu	Leu	Leu	Phe	Ser	Tyr	Ile	Ile
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Pro	Ile	Ser	Leu	Arg	Val	Asn	Leu	Asp	Met	Gly	Lys	Ala	Ala	Tyr	Gly
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Ser	Thr	Ile	Pro	Glu	Glu	Leu	Gly	Arg	Leu	Val	Tyr	Leu	Leu	Thr	Asp
				405					410					415	
Lys	Thr	Gly	Thr	Leu	Thr	Gln	Asn	Glu	Met	Val	Phe	Lys	Arg	Leu	His
			420					425					430		
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Thr	Gly	Glu	Thr	Glu	Phe	Ala	Glu	Ala	Asp	Gln	Asp	Phe	Ser	Asp	Glu
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Trp	Thr	Glu	Ser	Val	Gly	Leu	Thr	Leu	Val	Ser	Arg	Asp	Leu	Ala	Ser
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Met	Gln	Leu	Lys	Thr	Pro	Ser	Gly	Gln	Val	Leu	Thr	Tyr	Cys	Ile	Leu
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Gln	Met	Phe	Pro	Phe	Thr	Ser	Glu	Ser	Lys	Arg	Met	Gly	Ile	Ile	Val
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Arg	Asp	Glu	Ser	Thr	Ala	Glu	Ile	Thr	Phe	Tyr	Met	Lys	Gly	Ala	Asp
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Val	Ala	Met	Ser	Thr	Ile	Val	Gln	Tyr	Asn	Asp	Trp	Leu	Glu	Glu	Glu
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Leu Asn Ala Phe Arg Arg Lys His Asp Cys Ala Leu Val Ile Ser Gly
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 Leu Gly Cys Tyr Val Ala Ser Leu Ala Phe Leu Asn Glu Tyr Phe Gly
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<223> Xaa = Asp, Asn, or Ser

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<222> (2)
<223> Xaa = Gln, Glu, Asn, or Arg

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<222> (3)
<223> Xaa = Ser or Ala

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<222> (4)
<223> Xaa = Leu, Ile, Val, Ser, Ala, or Asn

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<223> Xaa = Leu, Ile, or Val

<220>
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<222> (6)
<223> Xaa = Thr, Ser, or Asn

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Xaa Xaa Xaa Asp Lys Thr Gly Thr Xaa Thr
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<210> 39

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<223> domain

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<222> (1)

<223> Xaa = Thr, Ile, or Val

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<223> Xaa = any amino acid

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<223> Xaa = Ala, Ser, or Gly

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<223> Xaa = Leu, Ile, Val, or Met

<220>

<221> VARIANT

<222> (7)

<223> Xaa = Thr or Ile

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Asp Lys Thr Gly Thr Xaa Xaa
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